

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) ANMELDER:

(A) NAME: Vasopharm Biotech GmbH & Co. KG
 (B) STREET: Leichtackerstr. 6
 (C) CITY: Veitshöchheim
 (D) STATE: Bayern
 (E) COUNTRY: Deutschland
 (F) POSTAL CODE: 97209

(ii) TITEL OF THE INVENTION: Isolated and purified human soluble
 guanylyl cyclase $\alpha 1/\beta 1$ (hsGCal/ $\beta 1$)

(iii) NUMBER OF SEQUENCES: 10

(iv) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) DATA TO SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3015 basepairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: doublestrand
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40	CCCTTATGGC	GATTGGGCGG	CTGCAGAGAC	CAGGACTCAG	TTCCCCTGCC	CTAGTCTGAG	60
	CCTAGTGGGT	GGGACTCAGC	TCAGAGTCAG	TTTTCCAGAA	GCAGGTTTCA	GTGCAGAGTT	120
	TTCTTACACT	TTTCTGCGC	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	GGCGGAGGAC	180
	ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGGCG	TGATCTCACC	240
	ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	CAGCCCCGAG	300
45	GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	GCCACCGCGG	360
	TCTCCGCGCC	TGTCTGCACC	CTGTGCGCTG	AGCTGCCTGA	CAGTGACAAT	GACATCCCAG	420
	TTACCAAGTG	CCTTGAATTG	ATAGTGGCTT	CTGTTTGTC	GTCTCATATA	AGAACTACAG	480
	CTCATCAGGA	GGAGATCGCA	GCAGGGTAAG	AGACACCAAC	ACCATGTTCT	GCACGAAGCT	540
	CAAGGATCTC	AAGATCACAG	GAGAGTGTC	TTTCTCCTTA	CTGGCACCAG	GTCAAGTTCC	600
50	TAACGAGTCT	TCAGAGGAGG	CAGCAGGAAG	CTCAGAGAGC	TGCAAAGCAA	CCGTGCCCCAT	660
	CTGTCAAGAC	ATTCTTGAGA	AGAACATACA	AGAAAGTCTT	CCTCAAAGAA	AAACCAGTCG	720
	GAGCCGAGTC	TATCTTCACA	CTTTGGCAGA	GAGTATTGTC	AAACTGATTT	TCCCAGAGTT	780
	TGAACGGCTG	AATGTTGCAC	TTCAGAGAAC	ATTGGCAAAG	CACAAAATAA	AAGAAAGCAG	840
	GAAATCTTTG	GAAAGAGAAG	ACTTTGAAAA	AACAATTGCA	GAGCAAGCAG	TTGCAGCAGG	900
55	AGTTCCAGTG	GAGGTTATCA	AAGAATCTCT	TGGTGAAGAG	GTTTTTAAAA	TATGTTACGA	960
	GGAAGATGAA	AACATCCTTG	GGGTGGTTGG	AGGCACCCTT	AAAGATTTTT	TAAACAGCTT	1020
	CAGTACCCTT	CTGAAACAGA	GCAGCCATTG	CCAAGAAGCA	GGAAAAAGGG	GCAGGCTTGA	1080
	GGACGCCTCC	ATTCTATGCC	TGGATAAGGA	GGATGATTTT	CTACATGTTT	ACTACTTCTT	1140
	CCCTAAGAGA	ACCACCTCCC	TGATTCTTCC	CGGCATCATA	AAGGCAGCTG	CTCAGCTATT	1200
60	ATATGAAACG	GAAGTGGAAG	TGTCGTTAAT	GCCTCCCTGC	TTCCATAATG	ATTGCAGCGA	1260
	GTTTGTTGAAT	CAGCCCTACT	TGTTGTACTC	CGTTCACATG	AAAAGCACCA	AGCCATCCCT	1320
	GTCCCCCAGC	AAACCCAGT	CCTCGCTGGT	GATTCCCACA	TCGCTATTCT	GCAAGACATT	1380

TCCATTCCAT TTCATGTTTG ACAAAGATAT GACAATTCTG CAATTTGGCA ATGGCATCAG 1440
 AAGGCTGATG AACAGGAGAG ACTTTCAAGG AAAGCCTAAT TTTGAAGAAT ACTTTGAAAT 1500
 TCTGACTCCA AAAATCAACC AGACGTTTAG CGGGATCATG ACTATGTTGA ATATGGACCT 1560
 TGTGTACGA GTGAGGAGAT GGGACAACTC TGTGAAGAAA TCTTCAAGGG TTATGGACCT 1620
 5 CAAAGGCCAA ATGATCTACA TTGTTGAATC CAGTGCATC TTGTTTTTGG GGTCACCCTG 1680
 TGTGGACAGA TTAGAAGATT TTACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATTCA 1740
 CAATGCACTG AGGGATGTGG TCTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCCTGAA 1800
 GAAGAGGCTG GGAAGCTGA AGGCTACCCCT TGAGCAAGCC CACCAAGCCC TGGAGGAGGA 1860
 GAAGAAAAAG ACAGTAGACC TTCTGTGCTC CATATTTCCC TGTGAGGTTG CTCAGCAGCT 1920
 10 GTGGCAAGGG CAAGTTGTGC AAGCCAAGAA GTTCAGTAAT GTCACCATGC TCTTCTCAGA 1980
 CATCGTTGGG TTTACTGCCA TCTGCTCCCA GTGCTCACCG CTGCAGGTCA TCACCATGCT 2040
 CAATGCACTG TACACTCGCT TCGACCAGCA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA 2100
 GACCATTGGC GATGCCTATT GTGTAGCTGG GGGATTACAC AAAGAGAGTG ATACTCATGC 2160
 TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC 2220
 15 CCATGGAGAA CCTATCAAGA TGCGAATTGG ACTGCACTCT GGATCAGTTT TTGCTGGCGT 2280
 CGTTGGAGTT AAAATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACCTC TGGCTAACAA 2340
 ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCAACAACCTT ACAGATTACT 2400
 CAAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAGG GAGGAACCTC CACCAAACTT 2460
 CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAACTC 2520
 20 AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT GCCAATTTTT TAGGCAAAGC 2580
 ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TGACTCATTG 2640
 AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA 2700
 AAATTTTCAGG AGCCAAGTCA CAATCTTTCT CCTGTTTAAAC ATGACAAAAT GTACTCACTT 2760
 CAGTACTTCA GCTCTTCAAG AAAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGAGTA 2820
 25 TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TTCAGCACCT TGTACATATA 2880
 TCAGATAATT GTAGTCAATT GTACAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT 2940
 GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCTG TCAAAAAAAAAA AAAAAAAAAA 3000
 AAAAAAAAAA AAAAA 3015

30

(2) DATA TO SEQ ID NO: 2:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 695 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase a1 (hsGCa1))
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

45 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro
 5 10 15
 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu
 20 25 30
 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln
 35 40 45
 50 Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr
 50 55 60
 Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys
 65 70 75 80
 55 Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr
 85 90 95
 Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu
 100 105 110
 Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Ala Ala Gly Val Pro
 115 120 125
 60 Val Glu Val Ile Lys Glu Ser Leu Gly Glu Glu Val Phe Lys Ile Cys
 130 135 140

	Tyr	Glu	Glu	Asp	Glu	Asn	Ile	Leu	Gly	Val	Val	Gly	Gly	Thr	Leu	Lys
	145					150					155					160
	Asp	Phe	Leu	Asn	Ser	Phe	Ser	Thr	Leu	Leu	Lys	Gln	Ser	Ser	His	Cys
				165						170					175	
5	Gln	Glu	Ala	Gly	Lys	Arg	Gly	Arg	Leu	Glu	Asp	Ala	Ser	Ile	Leu	Cys
				180					185					190		
	Leu	Asp	Lys	Glu	Asp	Asp	Phe	Leu	His	Val	Tyr	Tyr	Phe	Phe	Pro	Lys
		195						200					205			
10	Arg	Thr	Thr	Ser	Leu	Ile	Leu	Pro	Gly	Ile	Ile	Lys	Ala	Ala	Ala	His
	210					215						220				
	Val	Leu	Tyr	Glu	Thr	Glu	Val	Glu	Val	Ser	Leu	Met	Pro	Pro	Cys	Phe
	2225					230					235					240
	His	Asn	Asp	Cys	Ser	Glu	Phe	Val	Asn	Gln	Pro	Tyr	Leu	Leu	Tyr	Ser
				245						250					255	
15	Val	His	Met	Lys	Ser	Thr	Lys	Pro	Ser	Leu	Ser	Pro	Ser	Lys	Pro	Gln
				260					265					270		
	Ser	Ser	Leu	Val	Ile	Pro	Thr	Ser	Leu	Phe	Cys	Lys	Thr	Phe	Pro	Phe
		275						280					285			
20	His	Phe	Met	Phe	Asp	Lys	Asp	Met	Thr	Ile	Leu	Gln	Phe	Gly	Asn	Gly
	290					300						305				
	Ile	Arg	Arg	Leu	Met	Asn	Arg	Arg	Asp	Phe	Gln	Gly	Lys	Pro	Asn	Phe
	310					315					320					325
	Glu	Glu	Tyr	Phe	Glu	Ile	Leu	Thr	Pro	Lys	Ile	Asn	Gln	Thr	Phe	Ser
				330						335					340	
25	Gly	Ile	Met	Thr	Met	Leu	Asn	Met	Gln	Phe	Val	Val	Arg	Val	Arg	Arg
				345					350					355		
	Trp	Asp	Asn	Ser	Val	Lys	Lys	Ser	Ser	Arg	Val	Met	Asp	Leu	Lys	Gly
		360						365					370			
30	Gln	Met	Ile	Tyr	Ile	Val	Glu	Ser	Ser	Ala	Ile	Leu	Phe	Leu	Gly	Ser
	375					380						385				
	Pro	Cys	Val	Asp	Arg	Leu	Glu	Asp	Phe	Thr	Gly	Arg	Gly	Leu	Tyr	Leu
	390					395					400					405
	Ser	Asp	Ile	Pro	Ile	His	Asn	Ala	Leu	Arg	Asp	Val	Val	Leu	Ile	Gly
				410						415					420	
35	Glu	Gln	Ala	Arg	Ala	Gln	Asp	Gly	Leu	Lys	Lys	Arg	Leu	Gly	Lys	Leu
				425					430					435		
	Lys	Ala	Thr	Leu	Glu	Gln	Ala	His	Gln	Ala	Leu	Glu	Glu	Glu	Lys	Lys
		440						445					450			
40	Lys	Thr	Val	Asp	Leu	Leu	Cys	Ser	Ile	Phe	Pro	Cys	Glu	Val	Ala	Gln
	455					460						465				
	Gln	Leu	Trp	Gln	Gly	Gln	Val	Val	Gln	Ala	Lys	Lys	Phe	Ser	Asn	Val
	470					475					480					485
	Thr	Met	Leu	Phe	Ser	Asp	Ile	Val	Gly	Phe	Thr	Ala	Ile	Cys	Ser	Gln
				490						495					500	
45	Cys	Ser	Pro	Leu	Gln	Val	Ile	Thr	Met	Leu	Asn	Ala	Leu	Tyr	Thr	Arg
				505					510					515		
	Phe	Asp	Gln	Gln	Cys	Gly	Glu	Leu	Asp	Val	Tyr	Lys	Val	Glu	Thr	Ile
		520						525					530			
50	Gly	Asp	Ala	Tyr	Cys	Val	Ala	Gly	Gly	Leu	His	Lys	Glu	Ser	Asp	Thr
	535					540						545				
	His	Ala	Val	Gln	Ile	Ala	Leu	Met	Ala	Leu	Lys	Met	Met	Glu	Leu	Ser
	550					555					560					565
	Asp	Glu	Val	Met	Ser	Pro	His	Gly	Glu	Pro	Ile	Lys	Met	Arg	Ile	Gly
				570						575					580	
55	Leu	His	Ser	Gly	Ser	Val	Phe	Ala	Gly	Val	Val	Gly	Val	Lys	Met	Pro
				585					590					595		
	Arg	Tyr	Cys	Leu	Phe	Gly	Asn	Asn	Val	Thr	Leu	Ala	Asn	Lys	Phe	Glu
		600						605					610			
60	Ser	Cys	Ser	Val	Pro	Arg	Lys	Ile	Asn	Val	Ser	Pro	Thr	Thr	Tyr	Arg
	615						620					625				
	Leu	Leu	Lys	Asp	Cys	Pro	Gly	Phe	Val	Phe	Thr	Pro	Arg	Ser	Arg	Glu

630 635 640 645
 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe
 650 655 660
 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys
 665 670 675
 Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly
 680 685 690
 Ile Asp
 695

(2) DATA TO SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 basepairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: doublestrand
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25	CCCCCCCCCG	CCGCTGCCGC	CTCTGCCTGG	GTCCCTTCGG	CCGTACCTCT	GCGTGGGGGC	60
	TGCTTCCCCG	GCTCCCGGTG	CAGACACCAT	GTACGGATTT	GTGAATCACG	CCCTGGAGTT	120
	GCTGGTGATC	CGCAATTACG	GCCCCGAGGT	GTGGGAAGAC	ATCAAAAAAG	AGGCACAGTT	180
	AGATGAAGAA	GGACAGTTTC	TTGTCAGAAT	AATATATGAT	GACTCCAAAA	CTTATGATTT	240
	GGTTGCTGCT	GCAAGCAAAG	TCCTCAATCT	CAATGCTGGA	GAAATCCTCC	AAATGTTTGG	300
30	GAAGATGTTT	TTCGTCTTTT	GCCAAGAATC	TGGTTATGAT	ACAATCTTGC	GTGTCTCTGG	360
	CTCTAATGTC	AGAGAATTTT	TACAGAACCT	TGATGCTCTG	CACGACCACC	TTGCTACCAT	420
	CTACCCAGGA	ATGCGTGCAC	CTTCCTTTAG	GTGCACTGAT	GCAGAAAAGG	GCAAAGGACT	480
	CATTTTGCAC	TACTACTCAG	AGAGAGAAGG	ACTTCAGGAT	ATTGTCATTG	GAATCATCAA	540
	AACAGTGGCA	CAACAAATCC	ATGGCACTGA	AATAGACATG	AAGGTTATTC	AGCAAAGAAA	600
35	TGAAGAATGT	GATCATACTC	AATTTTTAAT	TGAAGAAAAA	GAGTCAAAAG	AAGAGGATTT	660
	TTATGAAGAT	CTTGACAGAT	TTGAAGAAAA	TGGTACCCAG	GAATCACGCA	TCAGCCCATA	720
	TACATTCTGC	AAAGCTTTTC	CTTTTCATAT	AATATTTGAC	CGGGACCTAG	TGGTCACTCA	780
	GTGTGGCAAT	GCTATATACA	GAGTTCTCCC	CCAGCTCCAG	CCTGGGAATT	GCAGCCTTCT	840
40	GTCTGTCTTC	TCGCTGGTTC	GTCCCTCATAT	TGATATTAGT	TTCCATGGGA	TCCTTTCTCA	900
	CATCAATACT	GTTTTTGTAT	TGAGAAGCAA	GGAAGGATTG	TTGGATGTGG	AGAAATTAGA	960
	ATGTGAGGAT	GAAGTACTG	GGACTGAGAT	CAGCTGCTTA	CGTCTCAAGG	GTCAAATGAT	1020
	CTACTTACCT	GAAGCAGATA	GCATACTTTT	TCTATGTTCA	CCAAGTGTCA	TGAACCTGGA	1080
	CGATTTGACA	AGGAGAGGGC	TGTATCTAAG	TGACATCCCT	CTGCATGATG	CCACGCGCGA	1140
	TCTTGTCTTT	TTGGGAGAAC	AATTTAGAGA	GGAATACAAA	CTCACCACAAG	AACTGGAAAT	1200
45	CCTCACTGAC	AGGCTACAGC	TCACGTTAAG	AGCCCTGGAA	GATGAAAAGA	AAAAGACAGA	1260
	CACATTGCTG	TATTCTGTCC	TTCTTCCGTC	TGTTGCCAAT	GAGCTGCGGC	ACAAGCGTCC	1320
	AGTGCCTGCC	AAAAGATATG	ACAATGTGAC	CATCCTCTTT	AGTGGCATTG	TGGGCTTCAA	1380
	TGCTTTCTGT	AGCAAGCATG	CATCTGGAGA	AGGAGCCATG	AAGATCGTCA	ACCTCCTCAA	1440
	CGACCTCTAC	ACCAGATTTG	ACACACTGAC	TGATTCCTGG	AAAAACCCAT	TTGTTTATAA	1500
50	GGTGGAGACT	GTTGGTGACA	AGTATATGAC	AGTGAGTGGT	TTACCAGAGC	CATGCATTCA	1560
	CCATGCACGA	TCCATCTGCC	ACCTGGCCTT	GGACATGATG	GAAATTGCTG	GCCAGGTTCA	1620
	AGTAGATGGT	GAATCTGTTC	AGATAACAAT	AGGGATACAC	ACTGGAGAGG	TAGTTACAGG	1680
	TGTCATAGGA	CAGCGGATGC	CTCGATACTG	TCTTTTTGGG	AATACTGTCA	ACCTCACAAG	1740
	CCGAACAGAA	ACCACAGGAG	AAAAGGGAAA	AATAAATGTG	TCTGAATATA	CATACAGATG	1800
55	TCTTATGTCT	CCAGAAAATT	CAGATCCACA	ATTCCACTTG	GAGCACAGAG	GCCCAGTGTC	1860
	CATGAAGGGC	AAAAAAGAAC	CAATGCAAGT	TTGGTTTCTA	TCCAGAAAAA	ATACAGGAAC	1920
	AGAGGAAACA	AAGCAGGATG	ATGACTGAAT	CTTGGATTAT	GGGGTGAAGA	GGAGTACAGA	1980
	CTAGGTTCCA	GTTTTCTCCT	AACACGTGCC	AAGCCCAGGA	GCAGTTCTTC	CCTATGGATA	2040
	CAGATTTTCT	TTTGTCCTTG	TCCATTACCC	CAAGACTTTC	TTCTAGATAT	ATCTCTCACT	2100
60	ATCCGTTATT	CAACCTTAGC	TCTGCTTTCT	ATTACTTTTT	AGGCTTTAGT	ATATTATCTA	2160
	AAGTTTGGCT	TTTGATGTGG	ATGATGTGAG	CTTCATGTGT	CTTAAAATCT	ACTACAAGCA	2220

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4:

20	Met	Tyr	Gly	Phe	Val	Asn	His	Ala	Leu	Glu	Leu	Leu	Val	Ile	Arg	Asn	
					5					10					15		
	Tyr	Gly	Pro	Glu	Val	Trp	Glu	Asp	Ile	Lys	Lys	Glu	Ala	Gln	Leu	Asp	
				20					25					30			
25	Glu	Glu	Gly	Gln	Phe	Leu	Val	Arg	Ile	Ile	Tyr	Asp	Asp	Ser	Lys	Thr	
			35					40					45				
	Tyr	Asp	Leu	Val	Ala	Ala	Ala	Ser	Lys	Val	Leu	Asn	Leu	Asn	Ala	Gly	
		50				55						60					
	Glu	Ile	Leu	Gln	Met	Phe	Gly	Lys	Met	Phe	Phe	Val	Phe	Cys	Gln	Glu	
		65				70					75					80	
30	Ser	Gly	Tyr	Asp	Thr	Ile	Leu	Arg	Val	Leu	Gly	Ser	Asn	Val	Arg	Glu	
					85					90					95		
	Phe	Leu	Gln	Asn	Leu	Asp	Ala	Leu	His	Asp	His	Leu	Ala	Thr	Ile	Tyr	
				100					105					110			
35	Pro	Gly	Met	Arg	Ala	Pro	Ser	Phe	Arg	Cys	Thr	Asp	Ala	Glu	Lys	Gly	
			115					120					125				
	Lys	Gly	Leu	Ile	Leu	His	Tyr	Tyr	Ser	Glu	Arg	Glu	Gly	Leu	Gln	Asp	
		130					135					140					
	Ile	Val	Ile	Gly	Ile	Ile	Lys	Thr	Val	Ala	Gln	Gln	Ile	His	Gly	Thr	
		145				150					155					160	
40	Glu	Ile	Asp	Met	Lys	Val	Ile	Gln	Gln	Arg	Asn	Glu	Glu	Cys	Asp	His	
					165					170					175		
	Thr	Gln	Phe	Leu	Ile	Glu	Glu	Lys	Glu	Ser	Lys	Glu	Glu	Asp	Phe	Tyr	
				180				185						190			
45	Glu	Asp	Leu	Asp	Arg	Phe	Glu	Glu	Asn	Gly	Thr	Gln	Glu	Ser	Arg	Ile	
		195						200					205				
	Ser	Pro	Tyr	Thr	Phe	Cys	Lys	Ala	Phe	Pro	Phe	His	Ile	Ile	Phe	Asp	
		210					215					220					
	Arg	Asp	Leu	Val	Val	Thr	Gln	Cys	Gly	Asn	Ala	Ile	Tyr	Arg	Val	Leu	
		225				230					235					240	
50	Pro	Gln	Leu	Gln	Pro	Gly	Asn	Cys	Ser	Leu	Ser	Ser	Val	Phe	Ser	Leu	
					245					250					255		
	Val	Arg	Pro	His	Ile	Asp	Ile	Ser	Phe	His	Gly	Ile	Leu	Ser	His	Ile	
				260				265						270			
55	Asn	Thr	Val	Phe	Val	Leu	Arg	Ser	Lys	Glu	Gly	Leu	Leu	Asp	Val	Glu	
		275						280					285				
	Lys	Leu	Glu	Cys	Glu	Asp	Glu	Leu	Thr	Gly	Thr	Glu	Ile	Ser	Cys	Leu	
		290					295					300					
	Arg	Leu	Lys	Gly	Gln	Met	Ile	Tyr	Leu	Pro	Glu	Ala	Asp	Ser	Ile	Leu	
		305				310					315						

Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
 340 345 350
 Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
 355 360 365
 5 Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu
 370 375 380
 Asp Glu Lys Lys Lys Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro
 385 390 395 400
 10 Ser Val Ala Asn Glu Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg
 405 410 415
 Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala
 420 425 430
 Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn
 435 440 445
 15 Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg
 450 455 460
 Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met
 465 470 475 480
 20 Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile
 485 490 495
 Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val
 500 505 510
 Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val
 515 520 525
 25 Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly
 530 535 540
 Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly
 545 550 555 560
 30 Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu
 565 570 575
 Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met
 580 585 590
 Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
 595 600 605
 35 Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp Asp
 610 615

(2) DATA TO SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCal)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro
 5 10

(2) DATA TO SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCb1)

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 6:

5 Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
 5 10 15
 Thr Gly Thr Glu Glu Thr
 20

10 (2) DATA TO SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 basepairs

(B) TYPE: nucleotide

15 (C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

20 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

25 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC

28

30

2) DATA TO SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 basepairs

35 (B) TYPE: nucleotide

(C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

40

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

45

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

ATTATGGAAG CAGGGAGG

18

50

2) DATA TO SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 basepairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: genomic DNA

60

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

5 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT

28

10 2) DATA TO SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 basepairs

(B) TYPE: nucleotide

15 (C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

20 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

25 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC

20